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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=1; day=8; hr=10; min=22; sec=40; ms=875;]

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Reviewer Comments:

Glu Leu Leu Asn Ser Met Asn. Ile Ser Gln Pro Thr Val Val Phe Val
115 120 125

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
370 375 380

Please delete invalid alpha numeric character appearing beside amino acid coding Asn at position 119 in the above sequence id# 39. Please also correct invalid amino acid numbering appearing above at position 375 in the sequence, please check the remaining sequences for similar errors.

Phe Lue Arg Ser Lue Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
275 280 285

Please also correct invalid amino acid coding Lue appearing at position 274 and 277 in the above sample of sequence id# 41.

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
65 70 75 80

Pro Ile Phe Gly ASn Gln Ile Xaa Pro Asp Thr Ala Ile Leu Ser Val
225 230 235 240

Per the above sample of sequence id# 42, please correct invalid amino acid numbering at position 75 in the sequence. Please also correct invalid amino acid coding ASn at position 229 in the sequence.

Application No: 09763824 Version No: 5.0

Input Set:**Output Set:**

Started: 2008-12-24 10:25:15.658
Finished: 2008-12-24 10:25:19.413
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 755 ms
Total Warnings: 36
Total Errors: 8
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2008-12-24 10:25:15.658
Finished: 2008-12-24 10:25:19.413
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 755 ms
Total Warnings: 36
Total Errors: 8
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 330	Invalid protein , found in SEQID(39) POS (119)Invalid
E 323	Invalid/missing amino acid numbering SEQID (39)at Protein (375)
E 323	Invalid/missing amino acid numbering SEQID (39) POS (376)
E 330	Invalid protein , found in SEQID(41) POS (274)Invalid Protein:Lue
E 330	Invalid protein , found in SEQID(41) POS (277)Invalid Protein:Lue
E 323	Invalid/missing amino acid numbering SEQID (42) POS (73)
E 323	Invalid/missing amino acid numbering SEQID (42)at Protein (75)
E 330	Invalid protein , found in SEQID(42) POS (229)Invalid Protein:ASn

<110> SQUIRRELL, DAVID J.
MURPHY, MELANIE J.
PRICE, RACHEL L.
LOWE, CHRISTOPHER R.
WHITE, PETER J.
TISI, LAURENCE C.
MURRAY, JAMES A. H .

<120> NOVEL ENZYME

<130> 1498-119

<140> 09763824

<141> 2001-02-27

<150> PCT/GB99/03538

<151> 1999-10-26

<150> GB 9823468.5

<151> 1998-10-28

<160> 42

<170> PatentIn Ver. 2.1

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 1

cgccggtgag ctccccgccg ccg

23

<210> 2

<211> 23

<212> DNA

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<223> Description of Artificial Sequence: Primer

<400> 2

cggcggcggg gagctcaccg gcg

23

<210> 3

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 3
cgaacacttc ttcacggtg accgccttaa gtctttaatt aaatacaaag g 51

<210> 4
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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cctttgtatt taattaaaga cttaaggcgg tcaactatga agaagtgttc g 51

<210> 5
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
gaaaggcccg gcaccagcct atcctctaga gg 32

<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
cctctagcgg ataggctggt gccgggcctt tc 32

<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
ccataaattt accgaattcg tcgacttcga tcgagg 36

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8	
gtgtggaatt gtgagcgg	18
<210> 9	
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gagatacgcc gcggttcctg g	21
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ccaggaaccg cggcgtatct c	21
<210> 11	
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ccctattttc attcctggcc aaaagcactc	30
<210> 12	
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gagtgcctttt ggccaggaat gaaaataggg	30
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<400> 13	
ccgcatagag ctctctgcgt cagattc	27

<210> 14
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 gaatctgacg cagagagctc tatgcgg 27

 <210> 15
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 15
 gttgaccgct tgggatacctt aattaaatac 30

 <210> 16
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 16
 gtatagattt gaaaaagagc tg 22

 <210> 17
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

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 cagctctttt tcaaattctat ac 22

 <210> 18
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 18
 ggctacatac tggagacata gc 22

 <210> 19

<211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 19
 gctatgtctc cagtatgtag cc 22

 <210> 20
 <211> 21
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 20
 gcagttgcgc ccgtgaacga c 21

 <210> 21
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 21
 gtcggttcacg ggcgcaactg c 21

 <210> 22
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 <212> DNA
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 <400> 22
 caaatcattc cgggtactgc gattttaag 29

 <210> 23
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
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 cttaaaatcg cagtaccgg aatgatttg 29

 <210> 24

<211> 27
 <212> DNA
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 <223> Description of Artificial Sequence: Primer

 <400> 24
 ccgcatagaa ctctctgcgt cagattc 27

 <210> 25
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 <210> 26
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 26
 ctgattacac ccaaggggga tg 22

 <210> 27
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 27
 catccccctt ggggtgtaatc ag 22

 <210> 28
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 <220>
 <221> modified_base
 <222> (15)..(17)
 <223> a, g, c or t

 <400> 28

cccttcgcga tagannngcc tgcgtcagt 29

<210> 29

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<220>

<221> modified_base

<222> (13)..(15)

<223> a, g, c or t

<400> 29

actgacgcag gcnnntctat gcggaaggg 29

<210> 30

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 30

gcaatcaaat cgctccggat actgc 25

<210> 31

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 31

gcagtatccg gagcgatttg attgc 25

<210> 32

<211> 20

<212> DNA

<213> Artificial Sequence

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<223>.Description of Artificial Sequence: Primer

<400> 32

ccattccatc aaggtttttg 20

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 33
 ccaaaacctt gatggaatgg 20

<210> 34
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 34
 aaacagggac ccatatggaa gacgc 25

<210> 35
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 35
 aattaactcg aggaatttcg tcacgctga atacag 36

<210> 36
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 36
 ccctattttc attcctggcc aaaagcactg 30

<210> 37
 <211> 550
 <212> PRT
 <213> Photinus pyralis

<400> 37
 Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro
 1 5 10 15
 Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
 20 25 30
 Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
 35 40 45
 Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
 50 55 60

Glu	Ala	Met	Lys	Arg	Tyr	Gly	Leu	Asn	Thr	Asn	His	Arg	Ile	Val	Val		65	70	75	80
Cys	Ser	Glu	Asn	Ser	Leu	Gln	Phe	Phe	Met	Pro	Val	Leu	Gly	Ala	Leu		85	90	95	
Phe	Ile	Gly	Val	Ala	Val	Ala	Pro	Ala	Asn	Asp	Ile	Tyr	Asn	Glu	Arg		100	105	110	
Glu	Leu	Leu	Asn	Ser	Met	Asn	Ile	Ser	Gln	Pro	Thr	Val	Val	Phe	Val		115	120	125	
Ser	Lys	Lys	Gly	Leu	Gln	Lys	Ile	Leu	Asn	Val	Gln	Lys	Lys	Leu	Pro		130	135	140	
Ile	Ile	Gln	Lys	Ile	Ile	Ile	Met	Asp	Ser	Lys	Thr	Asp	Tyr	Gln	Gly		145	150	155	160
Phe	Gln	Ser	Met	Tyr	Thr	Phe	Val	Thr	Ser	His	Leu	Pro	Pro	Gly	Phe		165	170	175	
Asn	Glu	Tyr	Asp	Phe	Val	Pro	Glu	Ser	Phe	Asp	Arg	Asp	Lys	Thr	Ile		180	185	190	
Ala	Leu	Ile	Met	Asn	Ser	Ser	Gly	Ser	Thr	Gly	Leu	Pro	Lys	Gly	Val		195	200	205	
Ala	Leu	Pro	His	Arg	Thr	Ala	Cys	Val	Arg	Phe	Ser	His	Ala	Arg	Asp		210	215	220	
Pro	Ile	Phe	Gly	Asn	Gln	Ile	Ile	Pro	Asp	Thr	Ala	Ile	Leu	Ser	Val		225	230	235	240
Val	Pro	Phe	His	His	Gly	Phe	Gly	Met	Phe	Thr	Thr	Leu	Gly	Tyr	Leu		245	250	255	
Ile	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	Tyr	Arg	Phe	Glu	Glu	Glu	Leu		260	265	270	
Phe	Leu	Arg	Ser	Leu	Gln	Asp	Tyr	Lys	Ile	Gln	Ser	Ala	Leu	Leu	Val		275	280	285	
Pro	Thr	Leu	Phe	Ser	Phe	Phe	Ala	Lys	Ser	Thr	Leu	Ile	Asp	Lys	Tyr		290	295	300	
Asp	Leu	Ser	Asn	Leu	His	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	Leu	Ser		305	310	315	320
Lys	Glu	Val	Gly	Glu	Ala	Val	Ala	Lys	Arg	Phe	His	Leu	Pro	Gly	Ile		325	330	335	
Arg	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Ile	Leu	Ile	Thr		340	345	350	
Pro	Glu	Gly	Asp	Asp	Lys	Pro	Gly	Ala	Val	Gly	Lys	Val	Val	Pro	Phe		355	360	365	

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys
530 535 540

Gly Gly Lys Ser Lys Leu
545 550

<210> 38

<211> 550

<212> PRT

<213> Photinus pyralis

<220>

<221> VARIANT

<222> (214)

<223> xaa=an amino acid other than Thr

<400> 38

Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro
1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
35 40 45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala

50		55		60	
Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val					
65		70		75	80
Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu					
	85		90		95
Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg					
	100		105		110
Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val Phe Val					
	115		120		125
Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro					
	130		135		140
Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly					
145		150		155	160
Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe					
	165		170		175
Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile					
	180		185		190
Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val					
	195		200		205
Ala Leu Pro His Arg Xaa Ala Cys Val Arg Phe Ser His Ala Arg Asp					
	210		215		220
Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val					
225		230		235	240
Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu					
	245		250		255
Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu					
	260		265		270
Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val					
	275		280		285
Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr					
	290		295		300
Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser					
305		310		315	320
Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile					
	325		330		335
Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr					
	340		345		350
Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe					

355		360		365
Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val				
370		375		380
Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly				
385		390		400
Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly				
	405		410	415
Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe				
	420		425	430
Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln				
	435		440	445
Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile				
	450		455	460
Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu				
465		470		480
Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys				
	485		490	495
Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu				
	500		505	510
Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly				
	515		520	525
Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys				
	530		535	540
Gly Gly Lys Ser Lys Leu				
545		550		
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				15
Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg				
	20		25	30
Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu				
	35		40	45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
100 105 110

Glu Leu Leu Asn Ser Met Asn. Ile Ser Gln Pro Thr Val Val Phe Val
115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
1